

GenCore version 5.1.5
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OM nucleic - nucleic search, using sw model

Run on: June 1, 2003, 15:21:24 ; Search time 2494.08 Seconds

(without alignments)
12850.800 Million cell updates/sec

Title: US-09-625-573-3
Perfect score: 19/19
Sequence: 1 CAGGACTGCCTGAGACAAGC.....ATATGCAATTAAATTAG 1979

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 10%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_estbaum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_ntcc:*

9: qb_est1:*

10: qb_est2:*

11: qb_ntcc:*

12: qb_est3:*

13: qb_est4:*

14: qb_est5:*

15: em_est5:*

16: em_estom:*

17: em_gss:*

18: em_gss_hum:*

19: em_gss_inv:*

20: em_gss_pnl:*

21: em_gss_vrt:*

22: em_gss_fun:*

23: em_gss_mam:*

24: em_gss_mus:*

25: em_gss_other:*

26: em_gss_pro:*

27: em_gss_rnd:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB	ID	Description
1	469.8	23.7	807	13	BI764263	BI764263 60304953
2	469	23.7	469	17	B84215	B84215 RPC111-22K6
3	357.6	18.1	487	10	BE656336	BE656336 UI-M-BH0-
4	326.2	16.5	542	9	AA547303	AA547303 vn28h04 r
5	296.4	15.0	480	10	AW657263	AW657263 109996 MA
6	292.6	14.8	447	9	AA671573	AA671573 v104g01.r

%
FEATURES source
SUMMARIES
RESULT 1
LOCUS BI764263 mRNA linear EST 25-SEP-2001
DEFINITION Homo sapiens clone IMAGE:5186388_5',
ORGANISM Homo sapiens
MATERIAL Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
ACCESSION BI764263 mRNA sequence.
VERSION BI764263.1
KEYWORDS EST
SOURCE Human.
ORGANISM Homo sapiens
MATERIAL Eukaryota; Metazoa; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 807)
AUTHORS N/A
TITLE OMIM http://mgc.ncbi.nlm.nih.gov/
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cstraps@nci.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGCG clone distribution information can be found through the LNL at:
http://image.llnl.gov
Plate: LIAM1465 row: 1 column: 13
High quality sequence stop: 805.
Location/Qualifiers 1 . 807

Db	241	GGGGAGGAAAGTCTGGTGGTTATAAACGAGGAAGCAGTTGATGTGTATTAA	300	Qy	151	TTCGATTATGATTACGGTGCCTCGTCAATAATTGACGTGAAAGCAAATTGGGCCAAC	210
Qy	1194	AGGGAGATAACATCTCTATATAACACAACACTTCAGGGTGTGACAATAGAAC	1253	Db	19	TCCATTAGGTGATGTCAGGACCTGGCAAAATTCAGACANAAATGCACTGTC	78
Db	301	AGGGAGATAACATCTCTATATAACACAACACTTCAGGGTGTGACAATAGAAC	360	Qy	211	TCCCTGCCCTCGCCTGCTACTCGCTGTGTCATCTGGGCAACATGCTGGTC	270
Qy	1254	TCTAAAGCTAGGTTGCCAGGAACCTCAGGCTGTGTGACTAACTACAGACTATGTCACCA	1313	Db	79	TCCCGCCCCACACTACGCTCTGTTGTTGTTGAACTATGTTGCT	138
Db	361	TGTAAGCTAGGTTGCCAGGAACCTCAGGCTGTGTGACTAACTACAGACTATGTCACCA	420	Qy	271	TCCCATCTTAACTAACTGCAAANAGCTGAAGCTCTGACTGACATTAACCTGTC	330
Qy	1314	ATGCCATATCCAAACATGCTCAGGAAATAATCCAGAAAAAACCTGGTTA	1362	Db	139	TCCCATCTTGATGAAAGTCGAAAPAGTCGAAATGCTGACTGATTCACCTGGTCAACC	198
Db	421	ATGCCATATCCAAACATGCTCAGGAAATAATCCAGAAAAAACCTGGTTA	469	Qy	331	TGGCATCTGATCTGCTGCTTCTTATTAATCTCCATTTGCTGACTCTGCAAC	390
				Db	199	TGGCATCTGATGCTGCTGCTGCTGCTGCTGACATACCACTCTGCTGACTCTGCA	258
RESULT	3			Qy	391	ATGAGTGGGTCCTTGGAAATGCAATTGCACTACAGGGTGTACATCGGT	450
LOCUS	BB656336	BB656336	487 bp mRNA linear EST 06-SEP-2000	Db	259	ATGAGTGGGTCCTTGGGATCATATGTPAAAGPATCACGGCTCATACATTGGT	318
DEFINITION	UT-M-BH0-aju-h-06-0-UI.r1	NIH_BMAP_M_S1	Mus musculus cDNA clone	Qy	451	ATTTGGGGAAATCTTCATCATCCCTCTGACAAATGGATAGATACCTGGCTATTGTCC	510
ACCESSION	BB656336	UT-M-BH0-aju-h-06-0-UI	5' mRNA sequence.	Db	319	ATTTGGGGAAATCTTCATCATCCCTCTGACAAATGGATAGATACCTGGCTATTGTCC	378
VERSION	BB656336.1	GR:982249		Qy	511	ATGCGTGTGTTGCTTAAAGCCAGGACGTCACCTTGGGTTGTGACAAGTGATCA	
KEYWORDS	EST.			Db	379	ATGCGTGTGTTGCTTAAAGCTGAACTGGTGTAACTTGGGTTATAACAGTGTGATCA	
SOURCE	house	mouse.		Qy	571	CCTGGTTGGGGTGTGCTGTGCTGTCAGGATCATCTTACTA	618
ORGANISM	Mus musculus	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		Db	439	CCTGGGGTGGTGGCTGTGTTGGCCCTCTCCAGAAATAATCTTACCA	486
REFERENCE	1	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus					
AUTHORS	Bonaldo,M.F., Lennon,G. and Soares,M.B.						
TITLE	Normalization and subtraction: two approaches to facilitate gene discovery						
JOURNAL	Genome Res. 6 (9), 791-806 (1996)						
MEDLINE	97044177						
COMMENT	Contact: Chin, H National Institute of Mental Health 6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD 20892-9643, USA Tel: 301 443 1706 Fax: 301 443 1706 Email: mEST@mail.nih.gov			RESULT	4		
CDNA Library Preparation:	M.B. Soares Lab Clone distribution: Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating small number of additional specialized non-redundant arrays of BMAP cDNAs whose availability will be conserved under appropriate and limited collaborative arrangements			LOCUS	AA547303	542 bp mRNA linear EST 05-AUG-1997	
RESEARCHERS	Site 1 to 487) Bonaldo,M.F., Lennon,G. and Soares,M.B. Normalization and subtraction: two approaches to facilitate gene discovery			DEFINITION	AA547303_r1	Soares_mammmary_gland_NbMMG	
FEATURES	Genome Res. 6 (9), 791-806 (1996)			IMAGE	vr28h04	MUS musculus cDNA clone	
Source	1. .487 'organism="Mus musculus" 'strain="C57BL/6J" '/db_xref="taxon:10090" '/clone="UT-M-BH0-aju-h-06-0-UI" '/clone_id="NIH_BMAP_M_S1" '/dev_stage="27-32 days" '/lab_host="DH10B (Life Technologies)" '/note="vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The NIH_BMAP_M_S1 library is a subtracted library derived from a mixture of normalized libraries from ten regions of the mouse brain (cerebellum, brain stems, olfactory bulbs, hypothalamus, cortex, amygdala, basal ganglia, pineal gland, striatum, hippocampus). The driver used for subtraction consisted of a pool of 20,000 cDNA clones obtained from non-normalized and normalized libraries of these ten regions of the mouse brain."			VERSION	GI:2308594		
BASE COUNT	115 a	115 c	103 g	KEYWORDS	AA547303	CHMOATTRACTANT PROTEIN 1 RECEPTOR ; mRNA sequence.	
ORIGIN				ORGANISM	AA547303	Mus musculus	
Query Match	Score 357.6;	DB 10;	Length 487;	REFERENCE	AA547303_1	Eukaryota; Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
Best Local Similarity	85.3%;	Pred. No. 7e-89;		AUTHORS	AA547303_1	1 (bases 1 to 542)	
Matches	Conservative 399;	Mismatches 69;	Indels 0;	JOURNAL	AA547303_1	Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.	
				COMMENT	AA547303_1	Unpublished (1996)	
				TITLE	AA547303_1	Contact: Marra M/Mouse EST Project	
				JOURNAL	AA547303_1	Washington University School of MedicineP	
				COMMENT	AA547303_1	4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108	
					AA547303_1	Tel: 314 286 1800	
					AA547303_1	Fax: 314 286 1810	
					AA547303_1	This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.lnl.gov) for further information.	
					AA547303_1	MGJ:544815	
					AA547303_1	High quality sequence stop: 286.	
					AA547303_1	Location/Qualifiers	
					AA547303_1	1. .542	
					AA547303_1	/organism="Mus musculus"	
					AA547303_1	/strain="C57BL/6J"	
					AA547303_1	/db_xref="taxon:10090"	
					AA547303_1	/clone="UT-M-BH0-aju-h-06-0-UI"	
					AA547303_1	/clone_id="NIH_BMAP_M_S1"	
					AA547303_1	/dev_stage="27-32 days"	
					AA547303_1	/lab_host="DH10B (Life Technologies)"	
					AA547303_1	/note="vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The NIH_BMAP_M_S1 library is a subtracted library derived from a mixture of normalized libraries from ten regions of the mouse brain (cerebellum, brain stems, olfactory bulbs, hypothalamus, cortex, amygdala, basal ganglia, pineal gland, striatum, hippocampus). The driver used for subtraction consisted of a pool of 20,000 cDNA clones obtained from non-normalized and normalized libraries of these ten regions of the mouse brain."	

RESULT 6		Db 122 ACTTGGGTATAACAGTAGTCATTTGGCTGCTCTCCAG 181
AA671573	LOCUS AA671573 r2 Soares_mammary_gland_NbMMG Mus musculus cDNA clone IMAGE:963216 5' similar to TR:GI1322040 G1322040 C-C CHEMOKINE RECEPTOR. ; mRNA sequence.	EST 25-NOV-1997
ACCESSION AA671573	VERSION AA671573.1 GI:2643652 EST.	RECEPTOR. ; mRNA sequence.
KEYWORDS	Mus musculus house mouse.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. (bases 1 to 447)
REFERENCE	AUTHORS Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.	EST published (1996)
TITLE	JOURNAL	The WashU-HMMI Mouse EST Project
COMMENT	Contract: Marra, M./Mouse EST Project	RESULT 7
	WashU-HMMI Mouse EST Project Washington University School of MedicineP 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108	BM917063
	Tel: 314 286 1800	LOCUS AGENCECOURT_6702060 NTM_MGC_106
	Fax: 314 286 1810	DEFINITION Homo sapiens cDNA clone IMAGE:5483554
	Email: mouseest@watson.wustl.edu	5', mRNA sequence.
	This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.	ACCESSION BM917063.1 GI:19367442
	MGIT:552008	ORGANISM Homo sapiens
	Seq. Primer: -28m13 rev2 ET from Amersham	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
	High quality sequence stop: 397.	REFERENCE 1. (bases 1 to 1074)
FEATURES	Location/Qualifiers 1..447	AUTHORS NIH-MGC http://mgc.nci.nih.gov/. TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
source	/organism="Mus musculus"	JOURNAL COMMENT Unpublished (1999)
	/strain="C57BL/6J"	TISSUE Procurement: Dr. Daniel McVICAR, DBS/NCI
	/db_xref="taxon:10090"	cDNA Library Preparation: Rubin Laboratory
	/clone="IMAGE:963216"	DNA Sequencing by: Agencourt Bioscience Corporation
	/clone.lib="Soares_mammary_gland_NBMMG"	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
	/sex="male"	Plate: LICM2011.row: 9 column: 11
	/tissue_type="mammary gland"	High quality sequence stop: 718.
	/dev_stage="4 weeks"	Location/Qualifiers
	/lab_host="DHL10B"	1..1074
	/note="Organ: mammary gland; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - Oligo(dT) primer [5' TGTACAATCTGAAGTGGAGCGGCCGATGGTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M. Fatima Bonaldo."	/tissue_type="natural killer cells, cell line"
ORIGIN	BASE COUNT 104 a 102 c 92 g 149 t	/lab_host="DHL10B (phage-resistant)" /note="Organ: blood; Vector: pOPIB7; Site_1: XbaI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XbaI sites using the following 5' adaptor: GGACCGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
		BASE COUNT 240 a 282 c 245 g 302 t 5 others
		Query Match 14.8% Score 292.6; DB 9; Length 447;
Best Local Similarity 80.7%; Conservative Matches 359;	Indels 12; Gaps 1;	Best Local Similarity 61.8%; Pred. No. 1.5e-69; Mismatches 0; Indels 301; Gaps 3;
QY 424 TATTCACTAGGGCTGTATACTACATGGTATTGGCGGAATCTCTCATCATCAGTCCTCGA 483		Query Match 14.6% Score 289; DB 14; Length 1074;
Db 2 TATTCACTAGGGCTGTATACTACATGGTATTGGCGGAATCTCTCATCATCAGTCCTCGA 61		Best Local Similarity 61.8%; Pred. No. 1.5e-69; Mismatches 0; Indels 18; Gaps 3;
QY 484 CAATCGATAGATACCTGGCTATGGCTATGGTGTGTTAACGCCAGACGGTCA 543		
Db 62 CATTGTGATAGGTACTTGCTATGGCTATGGCTATGGTGTGTTAACGCCAGACGGTCA 121		
QY 544 CCCTTGGGGTGGTGGTACCAAGTGTGATCACCTGGTGTGCTCTGTCAG 603		

Qy	141	ACCACCTTGTGATTAGTATACGGTGCCTGTCATAAATTGACGTGAGCAATT	200	JOURNAL MEDLINE	discovery
Db	63	ACCAAGAGTTGACTATGGATGCACTCCGGTGCAGAAGTGAACGGAGGGCCUT	122	COMMENT	Contact: Chin, H National Institute of Mental Health 6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD 20892-9643, USA Tel.: 301 443 1706 Fax: 301 443 9890 Email: mestr@mail.nih.gov
Qy	201	GGGGCCCAAATCCTCGCTCGGTCGTTGTTGTTGTTGGGGCAAC	260		The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bona fide poly A tail. The sequence tag present in the cDNA between the Nt site and the Oligo-dT track served to identify it as a clone from the normalized hypothalamus library: NIH_BMAP cDNA Library Preparation: M.B. Soares Lab Clone distribution: NIH_BMAP cDNA clones will be made available by the means that is soon to be determined. When NIH determines the means for distribution of the BMAP cDNA clones, this record will be updated accordingly when that means is determined.
Db	123	GGGGCCCAAATCCTCGCTCGGTCGTTGTTGTTGGGGCAAC	182		Seq Primer: M13 Forward
Qy	261	ATGGCTGGCTGCGCTCATCTTAAATGCAAAAAGCTGAACTGACATTTAC	320		POLY-A:Yes
Db	183	ATCCCTGGTGCGCTCGGTCGTTGCTACAGAGGTAAAAACATGCCAGCATTCAC	242	FEATURES	Location/Qualifiers
Qy	321	CTGCTCAACCTGGCCATCTCTGATGCTTTCCTATTACTCTCCCATTGGGGCTCAC	380	source	1. .452 /organism="Mus musculus" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="UTI-M-BHO-aju-h-06-0-UT" /clone.lib="NIH_BMAP_M_S1" /dev_stage="2-32 days" /lab_host="DH10B (Life Technologies)" /note="Vector: pET3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The NIH_BMAP_M_S1 library is a subtracted library derived from a mixture of normalized libraries from ten regions of the mouse brain (cerebellum, brain stems, olfactory bulbs, hypothalamus, cortex, amygdala, basal ganglia, pineal gland, striatum, hippocampus). The driver used for subtraction consisted of a pool of 20,000 cDNA clones obtained from non normalized and normalized libraries of these ten regions of the mouse brain. TAG_LIB-NIH_BMAP_M_S1 TAG_TISSUE="hypothalamus"
Db	243	CTCCCTAACCTGGCAATTCGACCTTCACCTGGCTTCTGGATGACAGTAC	497		TAG_SEQ-CGGTA
Qy	381	TCTGCTGCAA--ATGAGTGGCTCTGGATGCAATGCAAAATTCAGGGCTG	437		124 a 89 c 112 g 127 t
Db	303	TACAATGGAGGATGACTGGTTRITGGATGCGATGCTCGTGGSTTT	362		BASE COUNT ORIGIN
Qy	438	TATCACATCGGTATTTGGGAAATCTTCATCCCTGACATAGTAC	497		Query Match Best Local Similarity 14.4%; Score 284.8; DB 9; Matches 343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db	363	TATTACACAGCCTGTCACAGAGACTTTCATCCCTGTCAGATGACAGTAC	422		Length 452; pred. No. 1.7e-68;
Qy	498	CTGGGTATGGCCATCTGTGTTGGCTTACCTTGCTGGGTGGTG	557		
Db	423	CTGGGCATCTGCCACGCCGTTTGCCTGGCGACGTACTTGGGTGATC	482		
Qy	558	ACAAGTGTATCACCTGGCTTCTGCTGCCAGAAATCATCTTACT	617		
Db	483	ACCAGCATCATCATTTGGGCCTGGCCATCTGGCTTCCAGGTATATACTTTC	542		
Qy	618	AAATGCCAGAAAGAAAGNTCTGTTATGTTATGTTGTTGGCCCTTATTTT	665		
Db	543	AAGACCCAATGGGAATTCACTCACCACCTGCACTTCCTCAAGAAAGCCTA	602		
Qy	666	CGAGGATGGATAATTCCACAAATAATGAGAACATTTGGGGCTGCTGGCTG	725		
Db	603	CGAGAGTGGAGGAGMSUTTGGGCTTGAACTCTGGCTGGATTGCTTGG	662		
Qy	726	CTCATCATGGTCACTGGTCACTGGGAAATCTGAAACCTGTCGTCGAAACGAG	785		
Db	663	TTGGTCATGTCATGTCACAGGGATAATAAAGATTGCTAGACGCCAAATGAG	722		
Qy	786	AAGAAGGGCATGGCASTGAGATCATCTTCACATCATGATGTTACTTC	845		
Db	723	AAGAA---ATCCAAAGCTGCCGTTGATTTGTCATCATGATCATCTT	779		
Qy	846	TGGACTCCCTATAACATGTCATCTCCCTCAACACCTTCCAGGAATTCTGGCTGTAGT	905		
Db	780	TGGACCCCCATACATGACTATTTGACTATTTCTGTTTCCAGACTCTCC	839		
Qy	906	AACGTGAAAGCACCAGTAACATGTCATCTCCCTCAACACCTTCCAGGAATTCTGGCTGTAGT	961		
Db	840	GAGTGTGAGCAGCAGCATTTGACCTTGACCTGGCTGTGCAAGTGAACGAAATGATCG	895		
				RESULT 8	
LOCUS	AI851510	452 bp mRNA linear EST 15-JUL-1999		Qy	846 TGGACTCCCTATAACATGTCATCTCCCTCAACACCTTCCAGGAATTCTGGCTGTAGT 905
DEFINITION	UI-M-BHO-aju-h-06-0-UT. S2 NIH_BMAP_M_S1	Mus musculus cDNA clone		Db	331 TGGACTCCCTACAATGTCATCTGGCTGTAGT
ACCESSION	AI851510	mrna sequence		Qy	906 AACGTGAAAGCACCAGTAACATGTCATCTCCCTCAACACCTTCCAGGAATTCTGGCTGTAGT 961
VERSION	AI851510.1	EST.		Db	271 AACTGCACTGTTCTAAATGACTGACCCATGAGCTGCAAGTGAACGACTCTGGAAT 212
KEYWORDS		house mouse.			
SOURCE		Mus musculus			
ORGANISM		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus. 1 (bases 1 to 452)			
REFERENCE	Bonaldo, M.P., Lennon, G. and Soares, M.B.	Normalization and subtraction: two approaches to facilitate gene			
TITLE		CTCTCGGTGTTCTCCGAAAGCACATACCAAGCGCTCTGCACAAATGTCCAGTTTC	1085	Qy	1026

note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."

	Matches	448; Conservative	0; Mismatches	253; Indels	21; Gaps
Db	475	CTGGCCATTGTCACATCTGTGTTGCCCTTGAGCGGAGCTGTCACTTATGGTGTATC	534		
Qy	558	ACAAGTGTGATCACCGGTTGTTGCTGCTGCTGCCAGGAATCATCTTA	617		
Db	535	ACCGATCGCACCGGGCTGGCTAGTCAGCTCTGCAGTCATTTCTA	594		
Qy	618	AAATGCCAGAAAGATTCTGTTATGTCGTTGCCCTTATTTCACAGA-----	669		
Db	595	TGAGACTGAAAGTGTGAGACTCTTCGAGAGACTCTTCGAGTCATCAAGATAZAGCA	654		
Qy	670	---GATGGATAATTCCACACAAATAATGAGAACATTGGGGTCTGCCCTG	725		
Db	655	TATAGCTGGGGCATTTCACACTCTGAGAATGACATCTGCTTCCTCTG	714		
Qy	726	CTC-ATCATGGTCACTGCTGAAACCTGCTGCGTGTGAAACGA	784		
Db	715	CTCGTTCATGGCCATCTGCTGCAACAGGAGCTGCTGAGGTGCCCTGAA	774		
Qy	785	GAAGAGGGCATGGCAGTCAGTCATGATGTTACTTTCCTT	844		
Db	775	AACAAACAGTACAA-GCCATCCGGCTCAATTGGCCCATATGGCCGCTA-ACCATT	831		
Qy	845	CTGGACTCCCTATAACATGTCATCTCCT	874		
Db	832	CTGSGAACCCCTACATGTGGCTATCCCTCT	861		
RESULT 14					
BG182330	PG182330	884 bp mRNA linear EST 21-APR-2001			
DEFINITION	RST1196	Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.			
ACCESSION	BG182330				
VERSION	BG182330.1				
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
Mammalia; Butheroidea; Primates; Catarrhini; Hominoidea; Homo.					
1 (bases 1 to 884)					
REFERENCE	Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R., Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J., Lerner,L., Costanzo,D., McEligott,K., Boozer,S., Mays,R., Shih,E.B., Veloso,N., Klika,A., Hess,J., Offenbacher,J., Danzig,J. and Ducar,M.				
AUTHORS					
VERSION					
TITLE	Creation of genome-wide protein expression libraries using random activation of gene expression				
JOURNAL	Nat. Biotechnol. 19 (5), 440-445 (2001)				
COMMENT	Contact: Scott J. Cain				
FEATURES	High quality sequence stop: 529.				
source	Location/Qualifiers				
1. .884	/organism="Homo sapiens"				
/db_xref="taxon:9606"					
/clone.lib="Athersys RAGE Library"					
/cell.line="HT1080"					
/note="See 'Creation of Genome-wide Protein Expression, Libraries using Random Activation of Gene Expression, Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."					
BASE COUNT	191 a	Score 235.2; DB 12; Length 884;			
ORIGIN	231 c	Pred. No. 1.7e-54;			
Query Match	11.9%				
Best Local Similarity	62.0%				

Oncology Research
 University Health Network
 610 University Ave., 5-126, Toronto, Ontario, M5G 2M9, Canada
 Tel: (416) 946-4639
 Fax: (416) 946-6546
 Email: k.stewart@utoronto.ca
 PCR PRIMERS
 FORWARD: 5' -GCCAAGCTCGAAATTACCCCTCACTAAAGGG-3'
 BACKWARD: 5' -CCAGTGATTCATGAACTAACGACTCATATAAGGGC-3'
 Seq primer: 5'-GAATTAAACCCCTCACTAAAGGG-3'

FEATURES

source

Location/Qualifiers

Qualifiers

Source

1. .230
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone.lib="Myeloma (PCL) cDNA library"

/sex="male"
 /tissue_type="Blood"
 /cell_type="myeloma"

/dev_stage="Plasma cell leukemia"
 /note="Vector: Lambda Zap Express; Site_1: EcoRI; Site_2:
 XbaI; mRNA was purified from plasma cell leukemia
 patient's peripheral blood containing >95% myeloma. An
 oligo d(T)18 primer containing XbaI restriction site was
 used to prime first strand synthesis using M-MuLV reverse
 transcriptase. To protect the cDNAs from XbaI digestion in
 subsequent cloning step, the nucleotide analogue
 5-methyl-dCTP was added to the nucleotide mixture and
 [a-32P]dATP was added to monitor the quantity and quality
 of first strand synthesis. After second strand synthesis
 and blunting of cDNA termini, EcoRI adaptors were ligated
 followed by kinase treatment and digestion with XbaI.
 The cDNAs were then size-fractionated using Sephadryl
 S-500 column and then ligated into EcoRI and XbaI digested
 Lambda Zap Express vector. The ligation product was
 packaged using Gigapack II packaging extract. The library
 had primary titer of approx. 1x10⁶. Clones from the
 primary library were randomly selected for single pass
 sequencing."

BASE COUNT 67 a 53 C 45 g 65 t

ORIGIN

	Query	Match	Score	Length
Best	Matches	Local Similarity	DB 12;	230;
	230;	Conservative	Pred. No.	3e-53;
		0;	Mismatches	0;
			Indels	0;
			Gaps	0;
QY	1306	GTCACCCAAATGCAATATCCAAACATGTGCCTAGGAAATATCCAGAAAATCTGGTAGAG	1365	
Db	1	GTCAACCCAAATGCAATATCCAAACATGTGCCTAGGAAATATCCAGAAAATCTGGTAGAG	60	
QY	1366	ACTTTGACTCTCCAGAAAGCTCATCTAGCTCCTGAAATAATGCCCTCATTAACCTTGTGCTTA	1425	
Db	61	ACTTTGACTCTCCAGAAAGCTCATCTAGCTCCTGAAATAATGCCCTCATTAACCTTGTGCTTA	120	
QY	1486	ATCCTCTTTCTAGTCATTAATTCTTCACTCAATCTCTGATTCTGTCATGTCTG	1485	
Db	121	ATCCTCTTTCTAGTCATTAATTCTTCACTCAATCTCTGATCTGTCATGTCTG	180	
QY	1486	AAATCAAGGGCAGCTGGAGCTGAAAGAAGAATGTGCAAGSCACAGATG	1535	
Db	181	AAATCAAGGGCAGCTGGAGCTGAAAGAAGAATGTGCAAGSCACAGATG	230	

Search completed: June 1, 2003, 20:03:43
 Job time : 2502.08 secs



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